

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: December 13, 2004, 21:15:51 ; Search time 31 Seconds
(without alignments)
2731.315 Million cell updates/sec

Title: US-09-976-054-5
Perfect score: 588
Sequence: 1 cgtccgcgcccggccgacttc.....ggaatnntagataaaaaaant 440

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 566832

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+_n2p.model -DEV=xlp

-
Q=/cgn2_1/USPTO_spool_p/US09976054/runat_13122004_160520_24790/app_query.fasta_1
.583
-DB=PIR_79 -QFMT=fastan -SUFFIX=n2p.rpr -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09976054_@CGN_1_1_63_@runat_13122004_160520_24790 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	%					Description
	No.	Score	Match	Length	ID	
	1	169.5	28.8	183	1 S20867	adenine phosphorib
	2	169	28.7	223	2 G86399	protein F17L21.24
	3	157.5	26.8	181	2 T06263	adenine phosphorib
	4	156.5	26.6	182	2 T07636	adenine phosphorib
	5	153.5	26.1	183	2 T05451	adenine phosphorib
	6	129.5	22.0	192	1 S71272	adenine phosphorib
	7	116	19.7	183	2 AF0562	adenine phosphorib
	8	115	19.6	183	1 RTECA	adenine phosphorib
	9	111	18.9	181	2 G82246	adenine phosphorib
	10	110	18.7	183	2 B90694	adenine phosphorib
	11	110	18.7	183	2 F85544	adenine phosphorib
	12	100	17.0	187	2 AD0379	adenine phosphorib
	13	98	16.7	180	2 G64111	adenine phosphorib
	14	94.5	16.1	182	2 F83453	adenine phosphorib
	15	84.5	14.4	180	1 RTMSA	adenine phosphorib
	16	84.5	14.4	188	2 T38223	probable adenine p
	17	84	14.3	180	2 AC2851	adenine phosphorib
	18	84	14.3	182	2 F81366	adenine phosphorib
	19	84	14.3	198	2 A97628	adenine phosphorib
	20	80.5	13.7	180	2 S36334	adenine phosphorib
	21	77	13.1	172	2 S75440	adenine phosphorib
	22	76.5	13.0	173	2 G82883	adenine phosphorib
	23	76.5	13.0	180	1 RTHUA	adenine phosphorib
	24	76	12.9	79	2 A87553	hypothetical prote
	25	75.5	12.8	307	2 D83295	transaldolase PA27
	26	74	12.6	172	2 AF2378	adenine phosphorib
	27	74	12.6	186	2 AF3311	adenine phosphorib
c	28	73.5	11.8	550	2 T36746	probable serine/th
c	29	73	11.7	306	2 T06435	ribonuclease S5 ho
c	30	73	11.7	891	2 G84693	probable proline-r
	31	71.5	12.2	182	2 B49927	adenine phosphorib
	32	71	12.1	183	1 A29596	adenine phosphorib
	33	71	12.1	184	2 S34831	adenine phosphorib
	34	71	12.1	219	2 B84326	hypothetical prote
	35	70.5	12.0	264	2 JC6125	U2 small nuclear r
	36	70	11.9	163	2 D83850	inorganic pyrophos
c	37	69.5	11.2	200	2 T52627	splicing factor RS
c	38	69.5	11.2	200	2 T05112	splicing factor 9G
	39	68.5	11.6	503	2 F95988	probable ATP-depen
	40	67	11.4	158	2 T42700	hypothetical prote
c	41	66.5	10.7	198	2 A45067	laminin B1 chain v
c	42	66.5	10.7	287	2 E83398	hypothetical prote
c	43	66.5	10.7	431	2 S09824	hypothetical prote
c	44	66.5	10.7	1415	1 EDBEGA	immediate-early pr
c	45	66	10.6	649	2 JQ0103	hypothetical 70K p

ALIGNMENTS

RESULT 1

S20867

adenine phosphoribosyltransferase (EC 2.4.2.7) 1 [similarity] - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)
 C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
 C;Accession: S20867
 R;Moffatt, B.A.; McWhinnie, E.A.; Burkhardt, W.E.; Pasternak, J.J.; Rothstein, S.J.
 Plant Mol. Biol. 18, 653-662, 1992
 A;Title: A complete cDNA for adenine phosphoribosyltransferase from Arabidopsis thaliana.
 A;Reference number: S20867; MUID:92216042; PMID:1558943
 A;Accession: S20867
 A;Molecule type: mRNA
 A;Residues: 1-183 <MOF>
 A;Cross-references: UNIPROT:P31166; EMBL:X58640; NID:g16163; PIDN:CAA41497.1; PID:g16164
 A;Experimental source: strain cv.columbia
 A;Note: the authors translated the codon CTC for residue 138 as Ser
 A;Note: part of this sequence was confirmed by protein sequencing
 C;Genetics:
 A;Gene: apt; apt1
 C;Function:
 A;Pathway: purine salvage
 C;Superfamily: adenine phosphoribosyltransferase
 C;Keywords: glycosyltransferase; pentosyltransferase; salvage pathway

Alignment Scores:

Pred. No.:	8.41e-13	Length:	183
Score:	169.50	Matches:	42
Percent Similarity:	54.26%	Conservative:	9
Best Local Similarity:	44.68%	Mismatches:	41
Query Match:	28.83%	Indels:	2
DB:	1	Gaps:	1

US-09-976-054-5 (1-440) x S20867 (1-183)

Qy	115	GATGCGCGCTTGGCGNGATCGNCTCCTNCATCCNGGTNATNCCCGACTTNCCAAAGCCA	174
		::	
Db	8	AspProArgIleAlaLysIleAlaSerSerIleArgValIleProAspPheProLysPro	27
Qy	175	GGGATNATGTTTCAGGACATCANGANGNTGNTGTTTCGATCCCAAGGCGNTCCGTGACAAC	234
		:: ::	
Db	28	GlyIleMetPheGlnAspIleThrThrLeuLeuLeuAspThrGluAlaPheLysAspThr	47
Qy	235	ATATACCATTTTGTCAAGCGGTACAAGGACCAAGGNATCACCNCTGGAAANTAGGAGTTAA	294
		::: ::: :::	
Db	48	IleAlaLeuPheValAspArgTyrLysAspLysGlyIleSerVal-ValAlaGlyValG1	67
Qy	295	AGCTAGAGGGNTCANTTTCGGAACAACTANNTCTTANAANNAATTGGTCAAAAATNGGTG	354
		: ::	
Db	67	uAlaArgGlyPheIlePheGlyProProIleAlaLeuAlaIleGlyAlaLys---PheVa	86
Qy	355	NCNATTGAGGAAGCNNAATNAGNTGCCANGCNAAATGATT	394
		::: ::	
Db	86	1ProMetArgLysProLysLysLeuProGlyLysValIle	99

RESULT 2

G86399

protein F17L21.24 [imported] - Arabidopsis thaliana

RESULT 3

T06263

adenine phosphoribosyltransferase (EC 2.4.2.7) APT1 - wheat

C;Species: Triticum aestivum (common wheat)

C;Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 09-Jul-2004

C;Accession: T06263

R;Schnorr, K.S.; Moffatt, B.A.; Biget, E.; Laloue, M.

submitted to the EMBL Data Library, March 1995

A;Reference number: Z15574

A;Accession: T06263

A;Status: translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-181 <SCH>

A;Cross-references: UNIPROT:Q43199; EMBL:U22442; NID:g726304; PIDN:AAA80609.1;

PID:g726305

A;Experimental source: cv. Capitol, immature seeds, 23 days after flowering

C;Genetics:

A;Gene: APT1

C;Function:

A;Description: converts adenine to AMP

A;Pathway: purine salvage

C;Superfamily: adenine phosphoribosyltransferase

C;Keywords: glycosyltransferase; pentosyltransferase; salvage pathway

Alignment Scores:

Pred. No.:	2.66e-11	Length:	181
Score:	157.50	Matches:	39
Percent Similarity:	52.63%	Conservative:	11
Best Local Similarity:	41.05%	Mismatches:	43
Query Match:	26.79%	Indels:	2
DB:	2	Gaps:	1

US-09-976-054-5 (1-440) x T06263 (1-181)

Qy	112	GCTGATGCGCGCTTGGCGGNGATCGNCTCCTNCATCCNGGTNATNCCCGACTTNCCAAAG	171
		::: ::: :::	
Db	3	SerAspGlyArgValGluArgIleAlaSerSerIleArgAlaIleProAsnPheProLys	22
Qy	172	CCAGGGATNATGTTTCAGGACATCANGANGNTGNTGTTTCGATCCCAAGGCGNTCCGTGAC	231
		::: :::	
Db	23	ProGlyIleLeuPheGlnAspIleThrThrLeuLeuLeuAspProGlnAlaPheArgAsp	42
Qy	232	AACATATACCATTTTGTCAAGCGGTACAAGGACCAAGGNATCACCNATGGAAANTAGGAGT	291
		::: :::	
Db	43	ThrThrAspLeuPheValGluArgTyrLysAspLysAspIleThrVal-ValAlaGlyVa	62
Qy	292	TAAAGCTAGAGGGNTCANTTTTCGGAACAACACTANNTCTTANAANNAATTGGTCAAAAATNG	351
		::: :::	
Db	62	lGluAlaArgGlyPheIlePheGlyProProIleAlaLeuAlaIleGlyAlaLys---Ph	81
Qy	352	GTGNCNATTGAGGAAGCNNAATNAGNTGCCANGCNAAATGATT	394
		::: :::	
Db	81	eValProIleArgLysProLysLysLeuProGlyGluValIle	95

RESULT 4

T07636

C;Accession: S71272
R;Schnorr, K.M.; Laloue, M.; Hirel, B.
submitted to the EMBL Data Library, March 1996
A;Description: Isolation of cDNAs encoding two purine biosynthetic enzymes of soybean and expression of the corresponding transcripts in roots and root nodules.
A;Reference number: S71272
A;Accession: S71272
A;Molecule type: mRNA
A;Residues: 1-192 <SCH>
A;Cross-references: UNIPROT:Q42563; EMBL:X96866; NID:g1402893; PIDN:CAA65609.1; PID:g1321681
A;Experimental source: strain cv. columbia; isolate A19
C;Genetics:
A;Gene: apt2
A;Map position: 1
C;Function:
A;Pathway: purine salvage
C;Superfamily: adenine phosphoribosyltransferase
C;Keywords: glycosyltransferase; pentosyltransferase; salvage pathway

Alignment Scores:

Pred. No.:	8.36e-08	Length:	192
Score:	129.50	Matches:	37
Percent Similarity:	45.74%	Conservative:	6
Best Local Similarity:	39.36%	Mismatches:	49
Query Match:	22.02%	Indels:	2
DB:	1	Gaps:	1

US-09-976-054-5 (1-440) x S71272 (1-192)

Qy	115	GATGCGCGCTTGGCGGNGATCGNCTCCTNCATCCNGGTNATNCCCGACTTNCCAAAGCCA	174
Db	11	AspProArgLeuLysAlaIleSerAspAlaIleArgValIleProHisPheProLysThr	30
Qy	175	GGGATNATGTTTCAGGACATCANGANGNTGNTGTTTCGATCCCAAGGCGNTCCGTGACAAC	234
		:::	
Db	31	GlyIleMetPheGlnAspIleThrThrLeuLeuLeuAspProValAlaPheLysHisVal	50
Qy	235	ATATACCATTTTGTCAAGCGGTACAAGGACCAAGGNATCACNTGGAAANTAGGAGTTAA	294
		::: ::: :::	
Db	51	ValAspIlePheValAspArgTyrLysHisMetAsnIleSerLeu-ValAlaGlyValG1	70
Qy	295	AGCTAGAGGGNTCANTTTCGGAACAACACTANNTCTTANAANNAATTGGTCAAAAATNGGTG	354
		: :::	
Db	70	uAlaArgGlyPheIlePheGlyProProIleAlaLeuAlaIleGlyAlaLys---PheVa	89
Qy	355	NCNATTGAGGAAGCNNAATNAGNTGCCANGCNAAATGATT	394
		:::	
Db	89	lProLeuArgLysProGlyLysLeuProGlyArgValIle	102

RESULT 7

AF0562

adenine phosphoribosyltransferase [imported] - Salmonella enterica subsp. enterica serovar Typhi (strain CT18)

C;Species: Salmonella enterica subsp. enterica serovar Typhi

A;Note: this species has also been called Salmonella typhi

C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
 C;Accession: AF0562
 R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, C.; Mungall, K.L.; Bentley, S.D.; Holden, M.T.G.; Sebahia, M.; Baker, S.; Basham, D.; Brooks, K.; Chillingworth, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, J.; Feltwell, T.; Hamlin, N.; Haque, A.; Hien, T.T.; Holroyd, S.; Jagels, K.; Krogh, A.; Larsen, T.S.; Leather, S.; Moule, S.; O'Gaora, P.
 Nature 413, 848-852, 2001
 A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, B.G.
 A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhi CT18.
 A;Reference number: AB0502; MUID:21534947; PMID:11677608
 A;Accession: AF0562
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-183 <PAR>
 A;Cross-references: GB:AL513382; PIDN:CAD04968.1; PID:g16501754; GSPDB:GN00176
 C;Genetics:
 A;Gene: STY0527
 C;Superfamily: adenine phosphoribosyltransferase

Alignment Scores:

Pred. No.:	4.08e-06	Length:	183
Score:	116.00	Matches:	28
Percent Similarity:	52.78%	Conservative:	10
Best Local Similarity:	38.89%	Mismatches:	33
Query Match:	19.73%	Indels:	1
DB:	2	Gaps:	0

US-09-976-054-5 (1-440) x AF0562 (1-183)

Qy	103	ATGGCGTNCGCTGATGCGCGCTTGGCGGNGATCGNCTCCTNCATCCNGGTNATNCCCGAC	162
		:: ::: ::	
Db	1	MetThrAlaThrAlaGlnGlnLeuGluPheLeuLysAsnSerIleLysSerIleGlnAsp	20
Qy	163	TTNCCAAAGCCAGGGATNATGTTTCAGGACATCANGANGNTGNTGTTCGATCCCAAGGCG	222
		:: :: :: ::	
Db	21	TyrProLysProGlyIleLeuPheArgAspValThrSerLeuLeuGluAspProLysAla	40
Qy	223	NTCCGTGACAACATATAACATTTTGTCAAGCGGTACAAGGACCAAGGNATCACCNTGGAA	282
		::: ::: :::	
Db	41	TyrAlaLeuSerIleGluLeuLeuValGluArgTyrLysAsnAlaGlyIleThrLys-Va	60
Qy	283	ANTAGGAGTTAAAGCTAGAGGGNTCANTTTCGGA	316
		::	
Db	60	lValGlyThrGluAlaArgGlyPheLeuPheGly	71

RESULT 8

RTECA

adenine phosphoribosyltransferase (EC 2.4.2.7) - Escherichia coli (strain K-12)

N;Alternate names: AMP pyrophosphorylase; transphosphoribosidase

C;Species: Escherichia coli

C;Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 09-Jul-2004

C;Accession: A25635; B25549; D64777

R;Hershey, H.V.; Taylor, M.W.

Gene 43, 287-293, 1986

A;Title: Nucleotide sequence and deduced amino acid sequence of Escherichia coli adenine phosphoribosyltransferase and comparison with other analogous enzymes.

A;Reference number: A91548; MUID:86301884; PMID:3527873

A;Accession: A25635

A;Molecule type: DNA

A;Residues: 1-183 <HER>

A;Cross-references: UNIPROT:P07672; GB:M14040; GB:M25902; NID:g145293;

PIDN:AAA23455.1; PID:g145294

R;Flower, A.M.; McHenry, C.S.

Nucleic Acids Res. 14, 8091-8101, 1986

A;Title: The adjacent dnaZ and dnaX genes of Escherichia coli are contained within one continuous open reading frame.

A;Reference number: A25549; MUID:87040775; PMID:3534795

A;Accession: B25549

A;Molecule type: DNA

A;Residues: 40-183 <FLO>

A;Cross-references: GB:X04487; NID:g43319; PIDN:CAA28173.1; PID:g809695

R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.;

Riley, M.; Collado-Vides, J.; Glasner, J.D.; Rode, C.K.; Mayhew, G.F.; Gregor,

J.; Davis, N.W.; Kirkpatrick, H.A.; Goeden, M.A.; Rose, D.J.; Mau, B.; Shao, Y.

Science 277, 1453-1462, 1997

A;Title: The complete genome sequence of Escherichia coli K-12.

A;Reference number: A64720; MUID:97426617; PMID:9278503

A;Accession: D64777

A;Status: nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-183 <BLAT>

A;Cross-references: GB:AE000153; GB:U00096; NID:g1786671; PIDN:AAC73571.1;

PID:g1786675; UWGP:b0469

A;Experimental source: strain K-12, substrain MG1655

C;Genetics:

A;Gene: apt

A;Map position: 11 min

C;Function:

A;Pathway: purine salvage

C;Superfamily: adenine phosphoribosyltransferase

C;Keywords: glycosyltransferase; homodimer; pentosyltransferase; salvage pathway

Alignment Scores:

Pred. No.:	5.44e-06	Length:	183
Score:	115.00	Matches:	28
Percent Similarity:	52.78%	Conservative:	10
Best Local Similarity:	38.89%	Mismatches:	33
Query Match:	19.56%	Indels:	1
DB:	1	Gaps:	0

US-09-976-054-5 (1-440) x RTECA (1-183)

Qy	103	ATGGCGTNCGCTGATGCGCGCTTGGCGGNGATCGNCTCCTNCATCCNGGTNATNCCCGAC	162
		:: ::::	
Db	1	MetThrAlaThrAlaGlnGlnLeuGluTyrLeuLysAsnSerIleLysSerIleGlnAsp	20
Qy	163	TTNCCAAAGCCAGGGATNATGTTTCAGGACATCANGANGNTGNTGTTTCGATCCCAAGGCG	222
		:: :: ::	
Db	21	TyrProLysProGlyIleLeuPheArgAspValThrSerLeuLeuGluAspProLysAla	40

Qy 223 NTCCGTGACAACATATACCATTTTGTCAAGCGGTACAAGGACCAAGGNATCACCNTGGAA 282
 Db 41 TyrAlaLeuSerIleAspLeuLeuValGluArgTyrLysAsnAlaGlyIleThrLys-Va 60
 Qy 283 ANTAGGAGTTAAAGCTAGAGGGNTCANTTTTCGGA 316
 Db 60 lValGlyThrGluAlaArgGlyPheLeuPheGly 71

RESULT 9

G82246

adenine phosphoribosyltransferase VC1053 [imported] - Vibrio cholerae (strain N16961 serogroup O1)

C;Species: Vibrio cholerae

C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004

C;Accession: G82246

R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey, E.K.; Peterson, J.D.; Umayam, L.A.; Gill, S.R.; Nelson, K.E.; Read, T.D.; Tettelin, H.; Richardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, P.; McDonald, L.; Utterback, T.; Fleishmann, R.D.; Nierman, W.C.; White, O.; Salzberg, S.L.; Smith, H.O.; Colwell, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M. Nature 406, 477-483, 2000

A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.

A;Reference number: A82035; MUID:20406833; PMID:10952301

A;Accession: G82246

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-181 <HEI>

A;Cross-references: UNIPROT:Q9KT52; GB:AE004187; GB:AE003852; NID:g9655516; PIDN:AAF94212.1; GSPDB:GN00126; TIGR:VC1053

A;Experimental source: serogroup O1; strain N16961; biotype El Tor

C;Genetics:

A;Gene: VC1053

A;Map position: 1

C;Superfamily: adenine phosphoribosyltransferase

Alignment Scores:

Pred. No.:	1.72e-05	Length:	181
Score:	111.00	Matches:	26
Percent Similarity:	53.85%	Conservative:	9
Best Local Similarity:	40.00%	Mismatches:	29
Query Match:	18.88%	Indels:	1
DB:	2	Gaps:	0

US-09-976-054-5 (1-440) x G82246 (1-181)

Qy 124 TTGGCGGNGATCGNCTCCTNCATCCNGGTNATNCCCGACTTNCCAAAGCCAGGGATNATG 183
 Db 6 LeuSerLeuIleLysSerSerIleLysSerIleProAspTyrProLysLysGlyIleLeu 25
 Qy 184 TTTCAGGACATCANGANGNTGNTGTTCGATCCCAAGGCGNTCCGTGACAACATATACCAT 243
 Db 26 PheArgAspValThrSerLeuLeuGluAspAlaGlnAlaTyrGlnAlaThrIleGlnLeu 45
 Qy 244 TTTGTCAAGCGGTACAAGGACCAAGGNATCACCNTGGAAANTAGGAGTTAAAGCTAGAGG 303

Db 46 LeuValGluLysTyrLysAspMetGlyPheThrLys-ValValGlyThrGluAlaArgG1 65

Qy 304 GNTCANTTTCGGA 316

Db 65 yPheLeuPheGly 69

RESULT 10

B90694

adenine phosphoribosyltransferase [imported] - Escherichia coli (strain O157:H7, substrain RIMD 0509952)

C;Species: Escherichia coli

C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004

C;Accession: B90694

R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.; Ohtsubo, E.; Nakayama, K.; Murata, T.; Tanaka, M.; Tobe, T.; Iida, T.; Takami, H.; Honda, T.; Sasakawa, C.; Ogasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.

DNA Res. 8, 11-22, 2001

A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genomic comparison with a laboratory strain K-12.

A;Reference number: A99629; MUID:21156231; PMID:11258796

A;Accession: B90694

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-183 <HAY>

A;Cross-references: UNIPROT:Q8XD48; GB:BA000007; PIDN:BAB33945.1; PID:g13359979; GSPDB:GN00154

A;Experimental source: strain O157:H7, substrain RIMD 0509952

C;Genetics:

A;Gene: ECs0522

C;Superfamily: adenine phosphoribosyltransferase

Alignment Scores:

Pred. No.:	2.29e-05	Length:	183
Score:	110.00	Matches:	27
Percent Similarity:	51.39%	Conservative:	10
Best Local Similarity:	37.50%	Mismatches:	34
Query Match:	18.71%	Indels:	1
DB:	2	Gaps:	0

US-09-976-054-5 (1-440) x B90694 (1-183)

Qy 103 ATGGCGTNCGCTGATGCGCGCTTGGCGGNGATCGNCTCCTNCATCCNGGTNATNCCCGAC 162

Db 1 MetThrAlaThrAlaGlnGlnLeuGluTyrLeuLysAsnSerIleLysSerIleGlnAsp 20

Qy 163 TTNCCAAAGCCAGGGATNATGTTTTCAGGACATCANGANGNTGNTGTTTCGATCCCAAGGCG 222

Db 21 TyrProLysProGlyIleLeuPheArgAspValThrSerLeuLeuGluAspProLysAla 40

Qy 223 NTCCGTGACAACATATACCATTTTGTCAAGCGGTACAAGGACCAAGGNATCACCNATGGAA 282

Db 41 TyrAlaLeuSerIleAspLeuLeuValGluArgTyrLysAsnAlaGlyIleAsnLys-Va 60

Qy 283 ANTAGGAGTTAAAGCTAGAGGGNTCANTTTCGGA 316

Db 60 lValGlyThrGluAlaArgGlyPheLeuPheGly 71

RESULT 11

F85544

adenine phosphoribosyltransferase [imported] - Escherichia coli (strain 0157:H7, substrain EDL933)

C;Species: Escherichia coli

C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004

C;Accession: F85544

R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew, G.F.; Evans, P.S.; Gregor, J.; Kirkpatrick, H.A.; Posfai, G.; Hackett, J.; Klink, S.; Boutin, A.; Shao, Y.; Miller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, J.; Anantharaman, T.S.; Lin, J.; Yen, G.; Schwartz, D.C.; Welch, R.A.; Blattner, F.R.

Nature 409, 529-533, 2001

A;Title: Genome sequence of enterohemorrhagic Escherichia coli 0157:H7.

A;Reference number: A85480; MUID:21074935; PMID:11206551

A;Accession: F85544

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-183 <STO>

A;Cross-references: UNIPROT:Q8XD48; GB:AE005174; NID:g12513339; PIDN:AAG54818.1; GSPDB:GN00145; UWGP:Z0586

A;Experimental source: strain 0157:H7, substrain EDL933

C;Genetics:

A;Gene: apt

C;Superfamily: adenine phosphoribosyltransferase

Alignment Scores:

Pred. No.:	2.29e-05	Length:	183
Score:	110.00	Matches:	27
Percent Similarity:	51.39%	Conservative:	10
Best Local Similarity:	37.50%	Mismatches:	34
Query Match:	18.71%	Indels:	1
DB:	2	Gaps:	0

US-09-976-054-5 (1-440) x F85544 (1-183)

Qy	103	ATGGCGTNCGCTGATGCGCGCTTGGCGGNGATCGNCTCCTNCATCCNGGTNATNCCCGAC	162
		:: :: ::	
Db	1	MetThrAlaThrAlaGlnGlnLeuGluTyrLeuLysAsnSerIleLysSerIleGlnAsp	20
Qy	163	TTNCCAAAGCCAGGGATNATGTTTCAGGACATCANGANGNTGNTGTTTCGATCCCAAGGCG	222
		:: :: ::	
Db	21	TyrProLysProGlyIleLeuPheArgAspValThrSerLeuLeuGluAspProLysAla	40
Qy	223	NTCCGTGACAACATATAACCATTTTGTCAAGCGGTACAAGGACCAAGGNATCACCNCTGGAA	282
		:: :: ::	
Db	41	TyrAlaLeuSerIleAspLeuLeuValGluArgTyrLysAsnAlaGlyIleAsnLys-Va	60
Qy	283	ANTAGGAGTTAAAGCTAGAGGGNTCANTTTTCGGA	316
		::	
Db	60	lValGlyThrGluAlaArgGlyPheLeuPheGly	71

RESULT 12

AD0379

adenine phosphoribosyltransferase (EC 2.4.2.7) [imported] - Yersinia pestis (strain CO92)

C;Species: *Yersinia pestis*
 C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
 C;Accession: AD0379
 R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.;
 Prentice, M.B.; Sebahia, M.; James, K.D.; Churcher, C.; Mungall, K.L.; Baker,
 S.; Basham, D.; Bentley, S.D.; Brooks, K.; Cerdeno-Tarraga, A.M.; Chillingworth,
 T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; Feltwell, T.; Hamlin, N.;
 Holroyd, S.; Jagels, K.; Leather, S.; Karlyshev, A.V.; Moule, S.; Oyston,
 P.C.F.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
 Whitehead, S.; Barrell, B.G.
 Nature 413, 523-527, 2001
 A;Title: Genome sequence of *Yersinia pestis*, the causative agent of plague.
 A;Reference number: AB0001; MUID:21470413; PMID:11586360
 A;Accession: AD0379
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-187 <KUR>
 A;Cross-references: UNIPROT:Q8ZC94; GB:AL590842; PIDN:CAC92359.1; PID:g15981064;
 GSPDB:GN00175
 C;Genetics:
 A;Gene: apt
 C;Superfamily: adenine phosphoribosyltransferase
 C;Keywords: glycosyltransferase; pentosyltransferase

Alignment Scores:

Pred. No.:	0.000407	Length:	187
Score:	100.00	Matches:	24
Percent Similarity:	48.65%	Conservative:	12
Best Local Similarity:	32.43%	Mismatches:	37
Query Match:	17.01%	Indels:	1
DB:	2	Gaps:	0

US-09-976-054-5 (1-440) x AD0379 (1-187)

Qy	97	GTGGCGATGGCGTNCGCTGATGCGCGCTTGGCGGNGATCGNCTCCTNCATCCNGGTNATN	156
		::: ::: ::	
Db	3	ValSerAlaSerLysThrAlaGlnGlnLeuLysTyrIleLysAspSerIleLysThrIle	22
Qy	157	CCCGACTTNCCAAAGCCAGGGATNATGTTTCAGGACATCANGANGNTGNTGTTTCGATCCC	216
		:: ::: ::: ::	
Db	23	ProAspTyrProLysAlaGlyIleLeuPheArgAspValThrSerLeuLeuGluAsnPro	42
Qy	217	AAGGCGNTCCGTGACAACATATACCATTTTGTCAAGCGGTACAAGGACCAAGGNATCACC	276
		:: :: :: :::	
Db	43	LysAlaTyrSerAlaSerIleLysLeuLeuSerGluHisTyrSerGluSerGlyValThr	62
Qy	277	NTGGAAANTAGGAGTTAAAGCTAGAGGGNTCANTTTTCGGA	316
		::	
Db	63	Lys-ValValGlyThrGluAlaArgGlyPheLeuPheGly	75

RESULT 13

G64111

adenine phosphoribosyltransferase (EC 2.4.2.7) - *Haemophilus influenzae* (strain Rd KW20)

C;Species: *Haemophilus influenzae*
 C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 09-Jul-2004
 C;Accession: G64111

R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A.R.; Bult, C.J.; Tomb, J.F.; Dougherty, B.A.; Merrick, J.M.; McKenney, K.; Sutton, G.; FitzHugh, W.; Fields, C.; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.F.; Phillips, C.A.; Spriggs, T.; Hedblom, E.; Cotton, M.D.; Utterback, T.R.; Hanna, M.C.; Nguyen, D.T.; Saudek, D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.

Science 269, 496-512, 1995

A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, J.C.

A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.

A;Reference number: A64000; MUID:95350630; PMID:7542800

A;Accession: G64111

A;Status: nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-180 <TIGR>

A;Cross-references: UNIPROT:P43856; GB:U32802; GB:L42023; NID:g1574151;

PIDN:AAC22883.1; PID:g1574160; TIGR:HI1230

C;Genetics:

A;Gene: apt

C;Function:

A;Pathway: purine salvage

C;Superfamily: adenine phosphoribosyltransferase

C;Keywords: glycosyltransferase; pentosyltransferase; salvage pathway

Alignment Scores:

Pred. No.:	0.000724	Length:	180
Score:	98.00	Matches:	25
Percent Similarity:	54.55%	Conservative:	11
Best Local Similarity:	37.88%	Mismatches:	29
Query Match:	16.67%	Indels:	1
DB:	2	Gaps:	0

US-09-976-054-5 (1-440) x G64111 (1-180)

Qy 121 CGCTTGGCGGNGATCGNCTCCTNCATCCNGGTNATNCCCGACTTNCCAAAGCCAGGGATN 180
::||| ||| ||| ||| |||::| ||||| |||
Db 4 GlnLeuAspLeuIleLysSerSerIleLysSerIleProAsnTyrProLysGluGlyIle 23

Qy 181 ATGTTTCAGGACATCANGANGNTGNTGTTTCGATCCCAAGGCGNTCCGTGACAACATATAC 240
::|||:::||||| ||| ||| ::| |||
Db 24 IlePheArgAspIleThrThrLeuLeuGluValProAlaAlaPheLysAlaThrIleAsp 43

Qy 241 CATTTTGTCAAGCGGTACAAGGACCAAGGNATCACCNCTGGAAANTAGGAGTTAAAGCTAG 300
|||:::|:|||:::|:||| ||| ::::|
Db 44 LeuIleValGluGlnTyrArgAspLysGlyIleThrLys-ValLeuGlyThrGluSerAr 63

Qy 301 AGGGNTCANTTTTCGGA 316
||| |||||
Db 63 gGlyPheIlePheGly 68

RESULT 14

F83453

adenine phosphoribosyltransferase PA1543 [imported] - Pseudomonas aeruginosa (strain PA01)

C;Species: Pseudomonas aeruginosa

C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
 C;Accession: F83453
 R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Brinkman, F.S.L.; Hufnagle, W.O.; Kowalik, D.J.; Lagrou, M.; Garber, R.L.; Goltry, L.; Tolentino, E.; Westbrook-Wadman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, R.M.; Smith, K.A.; Spencer, D.H.; Wong, G.K.S.; Wu, Z.; Paulsen, I.T.; Reizer, J.; Saier, M.H.; Hancock, R.E.W.; Lory, S.; Olson, M.V.
 Nature 406, 959-964, 2000
 A;Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic pathogen.
 A;Reference number: A82950; MUID:20437337; PMID:10984043
 A;Accession: F83453
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-182 <STO>
 A;Cross-references: UNIPROT:Q04633; GB:AE004582; GB:AE004091; NID:g9947492; PIDN:AAG04932.1; GSPDB:GN00131; PASP:PA1543
 A;Experimental source: strain PAO1
 C;Genetics:
 A;Gene: apt; PA1543
 C;Superfamily: adenine phosphoribosyltransferase

Alignment Scores:

Pred. No.:	0.00198	Length:	182
Score:	94.50	Matches:	27
Percent Similarity:	45.45%	Conservative:	13
Best Local Similarity:	30.68%	Mismatches:	46
Query Match:	16.07%	Indels:	2
DB:	2	Gaps:	1

US-09-976-054-5 (1-440) x F83453 (1-182)

Qy	133	ATCGNCTCCTNCATCCNGGTNATNCCCGACTTNCCAAAGCCAGGGATNATGTTTCAGGAC	192
		::: ::: :::	
Db	8	LeuLysSerGlnIleArgAlaValProAspPheProLysProGlyValValPheArgAsp	27
Qy	193	ATCANGANGNTGNTGTTCGATCCCAAGGCGNTCCGTGACAACATATAACCATTTTGTCAAG	252
		::: :: :::	
Db	28	IleThrProLeuPheGlnSerProArgAlaLeuArgMetThrValAspSerPheValGln	47
Qy	253	CGGTACAAGGACCAAGGNATCACCNATGGAAANTAGGAGTTAAAGCTAGAGGGNTCANTTT	312
		:: :: ::	
Db	48	ArgTyrIleGluAlaAspPheSerHis-IleGlyAlaMetAspAlaArgGlyPheLeuIl	67
Qy	313	CGGAACAACCTANNTCTTANAANNAATTGGTCAAAAATNGGTGNCNATTGAGGAAGCNNA	372
		::: ::	
Db	67	eGlySerAlaValAla---TyrAlaLeuAsnLysProLeuValLeuPheArgLysGlnGl	86
Qy	373	TNAGNTGCCANGCNAATGATT	394
		:::::	
Db	86	yLysLeuProAlaAspValLeu	93

RESULT 15
 RTMSA
 adenine phosphoribosyltransferase (EC 2.4.2.7) - mouse

N;Alternate names: AMP pyrophosphorylase; gene APRT protein;
transphosphoribosidase
C;Species: Mus musculus (house mouse)
C;Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 09-Jul-2004
C;Accession: A22670; I49509
R;Dush, M.K.; Sikela, J.M.; Khan, S.A.; Tischfield, J.A.; Stambrook, P.J.
Proc. Natl. Acad. Sci. U.S.A. 82, 2731-2735, 1985
A;Title: Nucleotide sequence and organization of the mouse adenine
phosphoribosyltransferase gene: presence of a coding region common to animal and
bacterial phosphoribosyltransferases that has a variable intron/exon
arrangement.
A;Reference number: A22670; MUID:85190571; PMID:3921964
A;Accession: A22670
A;Molecule type: DNA
A;Residues: 1-180 <DUS>
A;Cross-references: UNIPROT:P08030; GB:M11310; NID:g192009; PIDN:AAA37255.1;
PID:g387103
R;Turker, M.S.; Cooper, G.E.; Bishop, P.L.
J. Mol. Evol. 36, 31-40, 1993
A;Title: Region-specific rates of molecular evolution: A fourfold reduction in
the rate of accumulation of silent mutations in transcribed versus
nontranscribed regions of homologous DNA fragments derived from two closely
related mouse species.
A;Reference number: I49509; MUID:93164265; PMID:8433377
A;Accession: I49509
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 63-107, 'VR', 108-133 <RES>
A;Cross-references: GB:M86439; NID:g192011; PIDN:AAA37256.1; PID:g553869
C;Comment: The active enzyme is a dimer of identical chains.
C;Genetics:
A;Gene: MGI:Appt
A;Cross-references: MGI:88061
A;Introns: 27/2; 63/1; 107/3; 134/1
C;Superfamily: adenine phosphoribosyltransferase
C;Keywords: glycosyltransferase; pentosyltransferase; salvage pathway

Alignment Scores:

Pred. No.:	0.0352	Length:	180
Score:	84.50	Matches:	23
Percent Similarity:	51.39%	Conservative:	14
Best Local Similarity:	31.94%	Mismatches:	31
Query Match:	14.37%	Indels:	4
DB:	1	Gaps:	1

US-09-976-054-5 (1-440) x RTMSA (1-180)

Qy	112	GCTGATGCGCGCTTGGCGGNGATCGNCTCCTNCATCCNGGTNATNCCCGACTTNCCAAAG	171
		::::: ::	
Db	2	SerGluProGluLeuLysLeuValAlaArgArgIleArgValPheProAspPheProIle	21
Qy	172	CCAGGGATNATGTTTCAGGACATCANGANGNTGNTGTTTCGATCCCAAGGCGNTCCGTGAC	231
		:: :: ::	
Db	22	ProGlyValLeuPheArgAspIleSerProLeuLeuLysAspProAspSerPheArgAla	41
Qy	232	AACATATAACCATTTTGTCAAGCGGTACAAGGACCAAGGNATCA-----CCNTGGAA	282
		:: :: :: ::::: :::	

Db 42 SerIle-ArgLeuLeuAlaSerHisLeuLysSerThrHisSerGlyLysIleAspTyrIl 61
Qy 283 ANTAGGAGTTAAAGCTAGAGGGNTCANTTTTCGGA 316
|||::: .:::||||| |||||
Db 61 eAlaGlyLeuAspSerArgGlyPheLeuPheGly 72

Search completed: December 13, 2004, 21:30:05
Job time : 34 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: December 13, 2004, 21:04:50 ; Search time 139 Seconds
(without alignments)
3642.660 Million cell updates/sec

Title: US-09-976-054-5
Perfect score: 588
Sequence: 1 cgtccgcgcccggccgacttc.....ggaatnntagataaaaaaant 440

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1825181-seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 3650362

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+_n2p.model -DEV=xlp
-Q=/cgn2_1/USPTO_spool_p/US09976054/runat_13122004_160519_
24784/app_query.fasta_1.583
-DB=UniProt_02 -QFMT=fastan -SUFFIX=n2p.rup -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09976054 @CGN_1_1_244 @runat_13122004_160519_24784 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query				
No.	Score	Match	Length	ID	Description

1	177.5	30.2	243	1	APT1_ARATH	P31166	arabidopsis
2	158.5	27.0	181	2	Q9LW89	Q9lw89	hordeum vul
3	158	26.9	204	2	Q7XJC2	Q7xjc2	brassica na
4	157.5	26.8	181	1	APT1_WHEAT	Q43199	triticum ae
5	156.5	26.6	178	2	Q8H0Y4	Q8h0y4	arabidopsis
6	156.5	26.6	182	2	Q9SU38	Q9su38	arabidopsis
7	153.5	26.1	183	2	Q8LG17	Q8lg17	arabidopsis
8	153.5	26.1	183	2	Q9SUW2	Q9suw2	arabidopsis
9	147.5	25.1	187	2	Q8H534	Q8h534	oryza sativ
10	141.5	24.1	191	2	Q9LFP0	Q9lfp0	arabidopsis
11	141.5	24.1	214	2	Q6RYT6	Q6ryt6	zea mays (m
12	141.5	24.1	214	2	AAR37033	Aar37033	zea mays
13	135.5	23.0	212	2	Q7X6S6	Q7x6s6	oryza sativ
14	135.5	23.0	212	2	Q84P57	Q84p57	oryza sativ
15	135.5	23.0	212	2	CAE02938	Cae02938	oryza sat
16	129.5	22.0	192	1	APT2_ARATH	Q42563	arabidopsis
17	129.5	22.0	192	2	AAL57714	Aal57714	arabidops
18	129.5	22.0	192	2	AAN64513	Aan64513	arabidops
19	126.5	21.5	238	2	Q6K5Y7	Q6k5y7	oryza sativ
20	126.5	21.5	238	2	BAD19719	Bad19719	oryza sat
21	119.5	20.3	213	2	Q6K5Y8	Q6k5y8	oryza sativ
22	119.5	20.3	213	2	BAD19718	Bad19718	oryza sat
23	118	20.1	177	1	APT_LEPIN	Q8exn2	leptospora
24	118	20.1	177	2	Q75FP0	Q75fp0	leptospora
25	118	20.1	177	2	AAS72170	Aas72170	leptospir
26	116.5	19.8	183	1	APT_SHIFL	Q83m42	shigella fl
27	116.5	19.8	183	2	Q7UDH7	Q7udh7	shigella fl
28	116	19.7	183	1	APT_SALTI	Q8z8t4	salmonella
29	116	19.7	183	1	APT_SALTY	Q8zra2	salmonella
30	115	19.6	181	1	APT_VIBVU	Q8db25	vibrio vuln
31	115	19.6	181	1	APT_VIBVY	Q7miv1	vibrio vuln
32	115	19.6	183	1	APT_ECOLI	P07672	escherichia
33	114	19.4	181	1	APT_VIBPA	Q87mq1	vibrio para
34	111.5	19.0	183	1	APT_PHOLL	Q7n0n9	photorhabdu
35	111	18.9	181	1	APT_VIBCH	Q9kt52	vibrio chol
36	110	18.7	183	1	APT_ECO57	Q8xd48	escherichia
37	108	18.4	174	2	Q6LTE9	Q6lte9	photobacter
38	108	18.4	174	2	CAG19427	Cag19427	photobact
39	108	18.4	180	1	APT_PASMU	P57841	pasteurella
40	108	18.4	185	2	Q6D800	Q6d800	erwinia car
41	100	17.0	187	1	APT_YERPE	Q8zc94	yersinia pe
42	98	16.7	171	1	APT_GLOVI	Q7ngz0	gloeobacter
43	98	16.7	180	1	APT_HAEIN	P43856	haemophilus
44	96	16.3	197	1	APT_RALSO	Q8y2b9	ralstonia s
45	94.5	16.1	179	1	APT_HAEDU	Q7vkq4	haemophilus

ALIGNMENTS

RESULT 1

APT1_ARATH

ID APT1_ARATH STANDARD; PRT; 243 AA.
AC P31166; Q8LGF6; Q9FZJ0;
DT 01-JUL-1993 (Rel. 26, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Adenine phosphoribosyltransferase 1 (EC 2.4.2.7) (APRT).
 GN Name=APT1; Synonyms=APT; OrderedLocusNames=Atlg27450;
 GN ORFNames=F17L21.24;
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 2).
 RC STRAIN=cv. Columbia;
 RX MEDLINE=92216042; PubMed=1558943;
 RA Moffatt B.A., McWhinnie E.A., Burkhart W.E., Pasternak J.J.,
 RA Rothstein S.J.;
 RT "A complete cDNA for adenine phosphoribosyltransferase from
 RT Arabidopsis thaliana.";
 RL Plant Mol. Biol. 18:653-662(1992).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM 2).
 RC STRAIN=cv. Columbia;
 RX MEDLINE=94266154; PubMed=8206375;
 RA Moffatt B.A., McWhinnie E.A., Agarwal S.K., Schaff D.A.;
 RT "The adenine phosphoribosyltransferase-encoding gene of Arabidopsis
 RT thaliana.";
 RL Gene 143:211-216(1994).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RX MEDLINE=21016719; PubMed=11130712; DOI=10.1038/35048500;
 RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,
 RA White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,
 RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
 RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,
 RA Dunn P., Etgu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,
 RA Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,
 RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
 RA Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,
 RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,
 RA Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziali A.,
 RA Militscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,
 RA Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
 RA Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
 RA Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,
 RA Utterback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M.,
 RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;
 RT "Sequence and analysis of chromosome 1 of the plant Arabidopsis
 RT thaliana.";
 RL Nature 408:816-820(2000).
 RN [4]
 RP SEQUENCE FROM N.A. (ISOFORM 2).
 RC STRAIN=cv. Columbia;
 RX MEDLINE=22954850; PubMed=14593172; DOI=10.1126/science.1088305;
 RA Yamada K., Lim J., Dale J.M., Chen H., Shinn P., Palm C.J.,
 RA Southwick A.M., Wu H.C., Kim C.J., Nguyen M., Pham P.K., Cheuk R.F.,
 RA Karlin-Newmann G., Liu S.X., Lam B., Sakano H., Wu T., Yu G.,
 RA Miranda M., Quach H.L., Tripp M., Chang C.H., Lee J.M., Toriumi M.J.,
 RA Chan M.M., Tang C.C., Onodera C.S., Deng J.M., Akiyama K., Ansari Y.,

RA Arakawa T., Banh J., Banno F., Bowser L., Brooks S.Y., Carninci P.,
RA Chao Q., Choy N., Enju A., Goldsmith A.D., Gurjal M., Hansen N.F.,
RA Hayashizaki Y., Johnson-Hopson C., Hsuan V.W., Iida K., Karnes M.,
RA Khan S., Koesema E., Ishida J., Jiang P.X., Jones T., Kawai J.,
RA Kamiya A., Meyers C., Nakajima M., Narusaka M., Seki M., Sakurai T.,
RA Satou M., Tamse R., Vaysberg M., Wallender E.K., Wong C., Yamamura Y.,
RA Yuan S., Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;
RT "Empirical analysis of transcriptional activity in the Arabidopsis
RT genome.";
RL Science 302:842-846(2003).
RN [5]

RP SEQUENCE FROM N.A. (ISOFORM 1).
RA Brover V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell R.,
RA Feldmann K.A.;
RT "Full-length cDNA from Arabidopsis thaliana.";
RL Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
CC -!- FUNCTION: Catalyzes a salvage reaction resulting in the formation
CC of AMP, that is energetically less costly than de novo synthesis.
CC -!- CATALYTIC ACTIVITY: AMP + diphosphate = adenine + 5-phospho-alpha-
CC D-ribose 1-diphosphate.
CC -!- PATHWAY: Purine salvage.
CC -!- SUBUNIT: Homodimer (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=P31166-1; Sequence=Displayed;
CC Note=No experimental confirmation available;
CC Name=2;
CC IsoId=P31166-2; Sequence=VSP_009002;
CC -!- SIMILARITY: Belongs to the purine/pyrimidine
CC phosphoribosyltransferase family.
CC -!- CAUTION: Ref.3 sequence differs from that shown due to erroneous
CC gene model prediction.
CC

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CC modified and this statement is not removed. Usage by and for
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CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC

DR EMBL; X58640; CAA41497.1; -.
DR EMBL; L19637; AAA20677.1; -.
DR EMBL; AC004557; AAF99737.1; ALT_SEQ.
DR EMBL; AF325045; AAG40397.1; -.
DR EMBL; AY128377; AAM91580.1; -.
DR EMBL; BT000370; AAN15689.1; -.

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DR      EMBL; AY084300; AAM60891.1; -.
DR      PIR; S20867; S20867.
DR      HSSP; P49435; 1G2P.
DR      InterPro; IPR005764; Ade_phospho_trans.
DR      InterPro; IPR002375; Pr/py_rp_transf.
DR      InterPro; IPR000836; PRtransferase.
DR      Pfam; PF00156; Pribosyltran; 1.
DR      TIGRFAMs; TIGR01090; apt; 2.
DR      PROSITE; PS00103; PUR_PYR_PR_TRANSFER; 1.
KW      Alternative splicing; Glycosyltransferase; Purine salvage;
KW      Transferase.
FT      VARSPLIC      1      60      Missing (in isoform 2).
FT                                     /FTId=VSP_009002.
SO      SEQUENCE      243 AA;  26396 MW;  92ABF089CA66C0FD CRC64;

```

Pred. No.:	2.64e-12	Length:	243
Score:	177.50	Matches:	48
Percent Similarity:	48.46%	Conservative:	15
Best Local Similarity:	36.92%	Mismatches:	51
Query Match:	30.19%	Indels:	16
DB:	1	Gaps:	2

Qy	49	GCTCCNNTGAGCGTGCGCGTACCGGCGGCAGGCGAGGGCAGGCGGTGGTGGCGATGGCG	108
		::: ::: :::::	
Db	32	AlaProProSerIleArgLeuSerAsnHisArgSerThrThrSerLeuArgLeuPheSer	51
Qy	109	TNCGCT-----GATGCGCGCTTG	126
		:::	
Db	52	SerAlaAlaAlaSerArgAspSerGluMetAlaThrGluAspValGlnAspProArgIle	71
Qy	127	GCGGNGATCGNCTCCTNCATCCNGGTNATNCCCGACTTNCCAAAGCCAGGGATNATGTTT	186
Db	72	AlaLysIleAlaSerSerIleArgValIleProAspPheProLysProGlyIleMetPhe	91
Qy	187	CAGGACATCANGANGNTGNTGTTTCGATCCCAAGGCGNTCCGTGACAACATATAACCATTTT	246
		:: ::	
Db	92	GlnAspIleThrThrLeuLeuLeuAspThrGluAlaPheLysAspThrIleAlaLeuPhe	111
Qy	247	GTCAAGCGGTACAAGGACCAAGGNATCACCN TGGAANTAGGAGTTAAAGCTAGAGGGNT	306
		::: ::: :::	
Db	112	ValAspArgTyrLysAspLysGlyIleSerVal-ValAlaGlyValGluAlaArgGlyPh	131
Qy	307	CANTTTTCGGAACA ACTANNTCTTANAANNAATTGGTCAAAAATNGGTGNCNATTGAGGAA	366
		::: :::	
Db	131	eIlePheGlyProProIleAlaLeuAlaIleGlyAlaLys---PheValProMetArgLy	150
Qy	367	GCNNAATNAGNTGCCANGCNAAATGATT	394
		:::	
Db	150	sProLysLysLeuProGlyLysValIle	159

Q9LW89


```

Qy      127 GCGGNGATCGNCTCCTNCATCCNGGTNATNCCCGACTTNCCAAAGCCAGGGATNATGTTT 186
          |||  |||  |||  |||  |||||  |||||  |||||  |||||
Db      32 ProLysIleAlaSerSerIleArgValIleProAspPheProLysProGlyIleMetPhe 51

Qy      187 CAGGACATCANGANGNTGNTGTTCGATCCCAAGGCGNTCCGTGACAACATATACCATTTT 246
          |||||  |||  ::|||  ::|||  |||  |||
Db      52 GlnAspIleThrThrLeuLeuLeuAspThrGluAlaPheLysAspThrIleAspIlePhe 71

Qy      247 GTCAAGCGGTACAAGGACCAAGGNATCACCNATGGAAANTAGGAGTTAAAGCTAGAGGGNT 306
          |||:::|||||||  :::|||||:::  |||||:::|||||||
Db      72 ValGluArgTyrLysCysLysGlyIleSerVal-ValAlaGlyValGluAlaArgGlyPh 91

Qy      307 CANTTTCGGAACAACACTANNTCTTANAANNAATTGGTCAAAAATNGGTGNCNATTGAGGAA 366
          |||||  :::  |||  :::|||||
Db      91 eIlePheGlyProProIleAlaLeuAlaIleGlyAlaLys---PheValProMetArgLy 110

Qy      367 GCNNAATNAGNTGCCANGCNAAATGATT 394
          |  |||  :::|
Db      110 sProLysLysLeuProGlyLysValIle 119

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RESULT 4

APT1_WHEAT

ID APT1_WHEAT STANDARD; PRT; 181 AA.

AC Q43199;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 01-OCT-2004 (Rel. 45, Last annotation update)

DE Adenine phosphoribosyltransferase 1 (EC 2.4.2.7) (APRT).

GN Name=APT1;

OS Triticum aestivum (Wheat).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;

OC Triticeae; Triticum.

OX NCBI_TaxID=4565;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=cv. Capitole; TISSUE=Seed;

RA Moffatt B.A., Schnorr K.S., Gaillard C., Biget E., Laloue M.;

RT "Nucleotide sequence of a wheat cDNA encoding adenine

phosphoribosyltransferase.";

RL (er) Plant Gene Register PGR95-030.

CC -!- FUNCTION: Catalyzes a salvage reaction resulting in the formation

CC of AMP, that is energetically less costly than de novo synthesis.

CC -!- CATALYTIC ACTIVITY: AMP + diphosphate = adenine + 5-phospho-alpha-

CC D-ribose 1-diphosphate.

CC -!- PATHWAY: Purine salvage.

CC -!- SUBUNIT: Homodimer (By similarity).

CC -!- SUBCELLULAR LOCATION: Cytoplasmic.

CC -!- SIMILARITY: Belongs to the purine/pyrimidine

CC phosphoribosyltransferase family.

CC

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CC or send an email to license@isb-sib.ch).
CC

DR EMBL; U22442; AAA80609.1; -.
DR PIR; T06263; T06263.
DR HSSP; P49435; 1G2Q.
DR InterPro; IPR005764; Ade_phospho_trans.
DR InterPro; IPR002375; Pr/py_rp_transf.
DR InterPro; IPR000836; PRtransferase.
DR Pfam; PF00156; Pribosyltran; 1.
DR TIGRFAMs; TIGR01090; apt; 1.
DR PROSITE; PS00103; PUR_PYR_PR_TRANSFER; 1.
KW Glycosyltransferase; Purine salvage; Transferase.
SQ SEQUENCE 181 AA; 19664 MW; 3325FBCF3780B24C CRC64;

Alignment Scores:

Pred. No.:	6.68e-10	Length:	181
Score:	157.50	Matches:	39
Percent Similarity:	52.63%	Conservative:	11
Best Local Similarity:	41.05%	Mismatches:	43
Query Match:	26.79%	Indels:	2
DB:	1	Gaps:	1

US-09-976-054-5 (1-440) x APT1_WHEAT (1-181)

QY	112	GCTGATGCGCGCTTGGCGNGATCGNCTCCTNCATCCNGGTNATNCCCGACTTNCCAAAG	171
		::: ::: :::	
Db	3	SerAspGlyArgValGluArgIleAlaSerSerIleArgAlaIleProAsnPheProLys	22
QY	172	CCAGGGATNATGTTTCAGGACATCANGANGNTGNTGTTTCGATCCCAAGGCGNTCCGTGAC	231
		::: :::	
Db	23	ProGlyIleLeuPheGlnAspIleThrThrLeuLeuLeuAspProGlnAlaPheArgAsp	42
QY	232	AACATATACCATTTTGTCAAGCGGTACAAGGACCAAGGNATCACCNATGGAAANTAGGAGT	291
		::: :::	
Db	43	ThrThrAspLeuPheValGluArgTyrLysAspLysAspIleThrVal-ValAlaGlyVa	62
QY	292	TAAAGCTAGAGGNTCANTTTCGGAACAACCTANNTCTTANAANNAATTGGTCAAAAATNG	351
		::: :::	
Db	62	lGluAlaArgGlyPheIlePheGlyProProIleAlaLeuAlaIleGlyAlaLys---Ph	81
QY	352	GTGNCNATTGAGGAAGCNNAATNAGNTGCCANGCNAAATGATT	394
		::: :::	
Db	81	eValProIleArgLysProLysLysLeuProGlyGluValIle	95

RESULT 5

Q8H0Y4

ID Q8H0Y4 PRELIMINARY; PRT; 178 AA.

AC Q8H0Y4;

Qy 355 NCNATTGAGGAAGCNNAATNAGNTGCCANGCNAAATGATT 394
 ||||| ||| ::|||
 Db 86 lProLeuArgLysProLysLysLeuProGlyGlnIleIle 99

RESULT 6

Q9SU38

ID Q9SU38 PRELIMINARY; PRT; 182 AA.
 AC Q9SU38;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Putative adenine phosphoribosyltransferase.
 GN Name=AT4g12440; Synonyms=At4g12440;
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA EU Arabidopsis sequencing project;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Yamada K., Chan M.M., Chang C.H., Dale J.M., Deng J.M., Hsuan V.W.,
 RA Lee J.M., Quach H.L., Tang C.C., Toriumi M., Wu H.C., Yu G.,
 RA Bowser L., Chen H., Cheuk R., Jones T., Karlin-Neumann G., Kim C.,
 RA Lam B., Lin J., Miranda M., Nguyen M., Palm C.J., Shinn P.,
 RA Southwick A., Davis R.W., Ecker J.R., Theologis A.;
 RL Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Peters S.A., van Staveren M., Dirkse W., Stiekema W., Mewes H.W.,
 RA Lemcke K., Mayer K.F.X.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
 CC -!- SIMILARITY: Belongs to the purine/pyrimidine
 CC phosphoribosyltransferase family.
 DR EMBL; AL049730; CAB41714.1; -.
 DR EMBL; AY133689; AAM91623.1; -.
 DR EMBL; AL161534; CAB78287.1; -.
 DR PIR; T07636; T07636.
 DR HSSP; P49435; 1G2Q.
 DR GO; GO:0003999; F:adenine phosphoribosyltransferase activity; IEA.
 DR GO; GO:0016757; F:transferase activity, transferring glycosyl. . .; IEA.
 DR GO; GO:0006168; P:adenine salvage; IEA.
 DR GO; GO:0009116; P:nucleoside metabolism; IEA.
 DR InterPro; IPR005764; Ade_phospho_trans.
 DR InterPro; IPR002375; Pr/py_rp_transf.
 DR InterPro; IPR000836; PRtransferase.
 DR Pfam; PF00156; Pribosyltran; 1.
 DR TIGRFAMs; TIGR01090; apt; 1.
 DR PROSITE; PS00103; PUR_PYR_PR_TRANSFER; 1.
 KW Glycosyltransferase; Transferase.
 SQ SEQUENCE 182 AA; 20355 MW; 976CA5085032935B CRC64;

Alignment Scores:

Pred. No.: 8.81e-10 Length: 182

Score:	156.50	Matches:	39
Percent Similarity:	53.19%	Conservative:	11
Best Local Similarity:	41.49%	Mismatches:	42
Query Match:	26.62%	Indels:	2
DB:	2	Gaps:	1

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Qy      115 GATGCGCGCTTGGCGGNATCGNCTCCTNCATCCNGGTNATNCCCGACTTNCCCAAAGCCA 174
        |||   |||:::   |||   :::   |||   |||   |||||   |||||
Db      8 AspProArgIleAspGlyIleLysThrLysIleArgValValProAspPheProLysLys 27

Qy     175 GGGATNATGTTTCAGGACATCANGANGNTGNTGTTCGATCCCCAAGGCGNTCCGTGACAAC 234
        |||   |||||||||||||||   ||||||||||||   ::|||
Db     28 GlyIleMetPheGlnAspIleThrThrLeuLeuLeuAspProLysAlaPheLysAspThr 47

Qy     235 ATATAACCATTTTGTC AAGCGGTACAAGGACCAAGGNATCACCN TGGAAANTAGGAGTTAA 294
        |||   |||||:::|||||:::|||   |||:::   |||:::
Db     48 IleAspLeuPheValGluArgTyrArgAspMetAsnIleSerVal-ValAlaGlyIleGl 67

Qy     295 AGCTAGAGGGNTCANTTTTCGGAACA ACTANNTCTTANAANNAATTGGTCAAAAATNGGTG 354
        :|||||||||   |||||:::   :: .   |||
Db     67 uAlaArgGlyPheIlePheGlySerProIleAlaLeuAlaIleGlyAlaLys---PheVa 86

Qy     355 NCNATTGAGGAAGCNNAATNAGNTGCCANGCNAAATGATT 394
        |||||||||   |||   ::|||
Db     86 lProLeuArgLysProLysLysLeuProGlyGlnIleIle 99
```

08LG17

RA Mayer K.F.X.;
 RL Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA EU Arabidopsis sequencing project;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Yamada K., Chan M.M., Chang C.H., Dale J.M., Hsuan V.W., Lee J.M.,
 RA Onodera C.S., Quach H.L., Tang C., Toriumi M., Wong C., Wu H.C.,
 RA Yu G., Yuan S., Carninci P., Chen H., Cheuk R., Hayashizaki Y.,
 RA Ishida J., Jones T., Kamiya A., Kawai J., Kim C.J., Narusaka M.,
 RA Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M., Shinn P.,
 RA Southwick A., Tripp M.G., Wu T., Shinozaki K., Davis R.W., Ecker J.R.,
 RA Theologis A.;
 RL Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Yamada K., Chan M.M., Chang C.H., Dale J.M., Hsuan V.W., Lee J.M.,
 RA Onodera C.S., Quach H.L., Tang C., Toriumi M., Wong C., Wu H.C.,
 RA Yu G., Yuan S., Carninci P., Chen H., Cheuk R., Hayashizaki Y.,
 RA Ishida J., Jones T., Kamiya A., Kawai J., Kim C.J., Narusaka M.,
 RA Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M., Shinn P.,
 RA Southwick A., Tripp M.G., Wu T., Shinozaki K., Davis R.W., Ecker J.R.,
 RA Theologis A.;
 RL Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RA Wedler H., Wambutt R., Mewes H.W., Lemcke K., Mayer K.F.X.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
 CC -!- SIMILARITY: Belongs to the purine/pyrimidine
 CC phosphoribosyltransferase family.
 DR EMBL; AL033545; CAA22162.1; -.
 DR EMBL; BT002969; AAO22778.1; -.
 DR EMBL; BT004412; AAO42406.1; -.
 DR EMBL; AL161557; CAB79212.1; -.
 DR PIR; T05451; T05451.
 DR HSSP; P49435; 1G2Q.
 DR GO; GO:0003999; F:adenine phosphoribosyltransferase activity; IEA.
 DR GO; GO:0016757; F:transferase activity, transferring glycosyl. . .; IEA.
 DR GO; GO:0006168; P:adenine salvage; IEA.
 DR GO; GO:0009116; P:nucleoside metabolism; IEA.
 DR InterPro; IPR005764; Ade_phospho_trans.
 DR InterPro; IPR002375; Pr/py_rp_transf.
 DR InterPro; IPR000836; PRtransferase.
 DR Pfam; PF00156; Pribosyltran; 1.
 DR TIGRFAMs; TIGR01090; apt; 1.
 DR PROSITE; PS00103; PUR_PYR_PR_TRANSFER; 1.
 KW Glycosyltransferase; Transferase.
 SQ SEQUENCE 183 AA; 20352 MW; F46139F77E31D20B CRC64;

Alignment Scores:

Pred. No.:	2.02e-09	Length:	183
Score:	153.50	Matches:	39
Percent Similarity:	52.13%	Conservative:	10
Best Local Similarity:	41.49%	Mismatches:	43
Query Match:	26.11%	Indels:	2

DB: 2 Gaps: 1

US-09-976-054-5 (1-440) x Q9SUW2 (1-183)

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Qy      115 GATGCGCGCTTGGCGGNGATCGNCTCCTNCATCCNGGTNATNCCCGACTTNCCAAAGCCA 174
          |||  |||:::  |||  :::  |||  |||  |||||  |||||
Db      9 AspProArgIleHisGlyIleLysThrLysIleArgValValProAspPheProLysLys 28

Qy      175 GGGATNATGTTTCAGGACATCANGANGNTGNTGTTTCGATCCCAAGGCGNTCCGTGACAAC 234
          |||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db      29 GlyIleMetPheGlnAspIleThrThrValLeuLeuAspProLysAlaPheLysAspThr 48

Qy      235 ATATACCATTTTGTCAAGCGGTACAAGGACCAAGGNATCACCNNTGGAAANTAGGAGTTAA 294
          |||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db      49 IleAspLeuPheValGluArgTyrArgAspLysAsnIleSerVal-ValAlaGlyIleGl 68

Qy      295 AGCTAGAGGGNTCANTTTCGGAACAACTANNTCTTANAANNAATTGGTCAAAAATNGGTG 354
          :|||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db      68 uAlaArgGlyPheLeuPheGlyProProIleAlaLeuAlaIleGlyAlaLys---PheVa 87

Qy      355 NCNATTGAGGAAGCNNAATNAGNTGCCANGCNAAATGATT 394
          |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db      87 lProLeuArgLysProLysLysLeuProGlyGluThrIle 100
```

RESULT 9

Q8H534

ID Q8H534 PRELIMINARY; PRT; 187 AA.
AC Q8H534;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Putative adenine phosphoribosyl transferase.
GN Name=OJ1753_E03.106;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RA Sasaki T., Matsumoto T., Yamamoto K.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
CC -!- SIMILARITY: Belongs to the purine/pyrimidine
CC phosphoribosyltransferase family.
DR EMBL; AP003849; BAC81171.1; -.
DR HSSP; P49435; 1G2P.
DR Gramene; Q8H534; -.
DR GO; GO:0003999; F:adenine phosphoribosyltransferase activity; IEA.
DR GO; GO:0016757; F:transferase activity, transferring glycosyl. . .; IEA.
DR GO; GO:0006168; P:adenine salvage; IEA.
DR GO; GO:0009116; P:nucleoside metabolism; IEA.
DR InterPro; IPR005764; Ade_phospho_trans.
DR InterPro; IPR002375; Pr/py_rp_transf.
DR InterPro; IPR000836; PRtransferase.
DR Pfam; PF00156; Pribosyltran; 1.
DR TIGRFAMs; TIGR01090; apt; 1.
DR PROSITE; PS00103; PUR_PYR_PR_TRANSFER; 1.

KW Glycosyltransferase; Transferase.
SQ SEQUENCE 187 AA; 20218 MW; 0DD0E1C633F3ECB2 CRC64;

Alignment Scores:

Pred. No.:	1.06e-08	Length:	187
Score:	147.50	Matches:	38
Percent Similarity:	51.11%	Conservative:	8
Best Local Similarity:	42.22%	Mismatches:	42
Query Match:	25.09%	Indels:	2
DB:	2	Gaps:	1

US-09-976-054-5 (1-440) x Q8H534 (1-187)

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Qy      115 GATGCGCGCTTGGCGGNGATCGNCTCCTNCATCCNGGTNATNCCCGACTTNCCAAAGCCA 174
          |||  |||      |||  |||  |||  |||  |||:::  ||| ||| |||
Db      12 AspProArgThrGlnAlaIleAlaSerThrIleArgValValProAsnPheProLysPro 31

Qy      175 GGGATNATGTTTCAGGACATCANGANGNTGNTGTTTCGATCCCAAGGCGNTCCGTGACAAC 234
          |||  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      32 GlyIleMetPheGlnAspIleThrThrLeuLeuLeuAsnProProValPheLysAspThr 51

Qy      235 ATATACCATTTTGTCAAGCGGTACAAGGACCAAGGNATCACNTGGAAANTAGGAGTTAA 294
          |||  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      52 IleAspLeuPheValGluArgTyrThrGlyLysGlyIleSerVal-ValAlaGlyValG1 71

Qy      295 AGCTAGAGGGNTCANTTTTCGGAACAACACTANNTCTTANAANNAATTGGTCAAAAATNGGTG 354
          :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      71 uAlaArgGlyPheIlePheGlyProProIleAlaLeuAlaIleGlyAlaLys---PheI1 90

Qy      355 NCNATTGAGGAAGCNNAATNAGNTGCCA 382
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      90 eProLeuArgLysProAsnLysLeuPro 99
```

RESULT 10

Q9LFP0

ID Q9LFP0 PRELIMINARY; PRT; 191 AA.
AC Q9LFP0;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Putative adenine phosphoribosyltransferase.
GN Name=F2I11_50; Synonyms=At5g11160;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Bevan M., Peters S.A., van Staveren M., Dirkse W., Stiekema W.,
RA Bancroft I., Mewes H.W., Rudd S., Lemcke K., Mayer K.F.X.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
RN [3]

RP SEQUENCE FROM N.A.
RA Yamada K., Chan M.M., Chang C.H., Dale J.M., Hsuan V.W., Lee J.M.,
RA Onodera C.S., Quach H.L., Tang C., Toriumi M., Wong C., Wu H.C.,
RA Yu G., Yuan S., Carninci P., Chen H., Cheuk R., Hayashizaki Y.,
RA Ishida J., Jones T., Kamiya A., Kawai J., Kim C.J., Narusaka M.,
RA Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M., Shinn P.,
RA Southwick A., Tripp M.G., Wu T., Shinozaki K., Davis R.W., Ecker J.R.,
RA Theologis A.;
RL Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Yamada K., Chan M.M., Chang C.H., Dale J.M., Hsuan V.W., Lee J.M.,
RA Onodera C.S., Quach H.L., Tang C., Toriumi M., Wong C., Wu H.C.,
RA Yu G., Yuan S., Carninci P., Chen H., Cheuk R., Hayashizaki Y.,
RA Ishida J., Jones T., Kamiya A., Kawai J., Kim C.J., Narusaka M.,
RA Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M., Shinn P.,
RA Southwick A., Tripp M.G., Wu T., Shinozaki K., Davis R.W., Ecker J.R.,
RA Theologis A.;
RL Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
CC -!- SIMILARITY: Belongs to the purine/pyrimidine ,
CC phosphoribosyltransferase family.
DR EMBL; AL360314; CAB96651.1; -.
DR EMBL; BT004028; AAO42064.1; -.
DR EMBL; BT005077; AAO50610.1; -.
DR HSSP; P49435; 1G2P.
DR GO; GO:0003999; F:adenine phosphoribosyltransferase activity; IEA.
DR GO; GO:0016757; F:transferase activity, transferring glycosyl. . .; IEA.
DR GO; GO:0006168; P:adenine salvage; IEA.
DR GO; GO:0009116; P:nucleoside metabolism; IEA.
DR InterPro; IPR005764; Ade_phospho_trans.
DR InterPro; IPR002375; Pr/py_rp_transf.
DR InterPro; IPR000836; PRtransferase.
DR Pfam; PF00156; Pribosyltran; 1.
DR TIGRFAMs; TIGR01090; apt; 1.
DR PROSITE; PS00103; PUR_PYR_PR_TRANSFER; 1.
KW Glycosyltransferase; Transferase.
SQ SEQUENCE 191 AA; 20757 MW; EC202C6FBD858E78 CRC64;

Alignment Scores:

Pred. No.:	5.57e-08	Length:	191
Score:	141.50	Matches:	39
Percent Similarity:	50.00%	Conservative:	8
Best Local Similarity:	41.49%	Mismatches:	45
Query Match:	24.06%	Indels:	2
DB:	2	Gaps:	1

US-09-976-054-5 (1-440) x Q9LFP0 (1-191)

Qy	115	GATGCGCGCTTGGCGGNGATCGNCTCCTNCATCCNGGTNATNCCCGACTTNCCAAAGCCA	174
		::: :::	
Db	11	AspProArgLeuGluAlaIleSerAlaAlaIleArgValValProAsnPheProLysLys	30
Qy	175	GGGATNATGTTTCAGGACATCANGANGNTGNTGTTTCGATCCCAAGGCGNTCCGTGACAAC	234
		:::	
Db	31	GlyIleMetPheGlnAspIleThrThrLeuLeuLeuAspHisLysAlaPheLysHisThr	50
Qy	235	ATATACCATTTTGTCAAGCGGTACAAGGACCAAGGNATCACCNATGGAAANTAGGAGTTAA	294

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Db      51  |||  |||||  |||||  |||||  |||:::  |||||::
Qy      295 AGCTAGAGGGNTCANTTTTCGGAACAACCTANNTCTTANAANNAATTGGTCAAAAATNGGTG 354
      :|||  |||||  |||||  ::  ::  |||
Db      70  uAlaArgGlyPheLeuPheGlyProSerIleAlaLeuAlaIleGlyAlaLys---PheIl 89
Qy      355 NCNATTGAGGAAGCNNAATNAGNTGCCANGCNAAATGATT 394
      |||||  |||  ::|||
Db      89  eProLeuArgLysProGlyLysLeuProGlyLysValIle 102

```

RESULT 11

Q6RYT6

```

ID  Q6RYT6      PRELIMINARY;      PRT;      214 AA.
AC  Q6RYT6;
DT  05-JUL-2004 (TrEMBLrel. 27, Created)
DT  05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT  05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE  Adenine phosphoribosyltransferase.
GN  Name=apt1;
OS  Zea mays (Maize).
OC  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC  Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC  PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX  NCBI_TaxID=4577;
RN  [1]
RP  SEQUENCE FROM N.A.
RA  Yu Z., Kong F., Ye C., Liang F., Yang J., Zheng G., Wang B.;
RL  Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases.
CC  -!- SIMILARITY: Belongs to the purine/pyrimidine
CC  phosphoribosyltransferase family.
DR  EMBL; AY485263; AAR37033.1; -.
DR  GO; GO:0016757; F:transferase activity, transferring glycosyl. . .; IEA.
DR  InterPro; IPR005764; Ade_phospho_trans.
DR  InterPro; IPR002375; Pr/py_rp_transf.
DR  InterPro; IPR000836; PRtransferase.
DR  Pfam; PF00156; Pribosyltran; 1.
DR  TIGRFAMs; TIGR01090; apt; 1.
DR  PROSITE; PS00103; PUR_PYR_PR_TRANSFER; 1.
KW  Glycosyltransferase; Transferase.
SQ  SEQUENCE      214 AA;  22705 MW;  63BA4C4560D0B945 CRC64;

```

Alignment Scores:

Pred. No.:	5.56e-08	Length:	214
Score:	141.50	Matches:	36
Percent Similarity:	46.32%	Conservative:	8
Best Local Similarity:	37.89%	Mismatches:	49
Query Match:	24.06%	Indels:	2
DB:	2	Gaps:	1

US-09-976-054-5 (1-440) x Q6RYT6 (1-214)

```

Qy      100 GCGATGGCGTNCGCTGATGCGCGCTTGGCGGNGATCGNCTCCTNCATCCNGGTNATNCCC 159
      :::::  |||||  |||||  |||  |||  |||
Db      34  SerLeuGlyAlaAlaAspProArgLeuGlnAlaIleSerAspAlaIleArgValValPro 53
Qy      160 GACTTNCCAAAGCCAGGGATNATGTTTCAGGACATCANGANGNTGNTGTTTCGATCCCAAG 219

```

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          ||||| ||||| ||||| |||
Db      54 HisPheProLysProGlyIleMetPheAsnAspIleThrGluLeuLeuLeuArgProGly 73
QY      220 GCGNTCCGTGACAACATATACCATTTTGTCAAGCGGTACAAGGACCAAGGNATCACCNTG 279
          ||||| ::: |||||:::|||||::: |||||
Db      74 ValPheArgAspAlaValAspMetPheValGluArgTyrArgGlyMetGlyIleAlaAla 93
QY      280 GAAANTAGGAGTTAAAGCTAGAGGGNTCANTTTCGGAACAACTANNTCTTANAANNAATT 339
          |||:::||||||| ||||| :::
Db      94 -AlaAlaGlyIleGluAlaArgGlyPheIlePheGlyProAlaIleAlaLeuAlaIleGl 113
QY      340 GGTCAAAAATNGGTGNCNATTGAGGAAGCNNAATNAGNTGCCA 382
          ||| ||||| |||
Db      113 yAlaLys---PheIleProLeuArgLysProLysLysLeuPro 126

```

RESULT 12

AAR37033

```

ID   AAR37033      PRELIMINARY;          PRT;    214 AA.
AC   AAR37033;
DT   02-MAR-2004 (TrEMBLrel. 27, Created)
DT   02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT   02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE   Adenine phosphoribosyltransferase.
GN   APT1.
OS   Zea mays (Maize).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC   PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX   NCBI_TaxID=4577;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Yu Z., Kong F., Ye C., Liang F., Yang J., Zheng G., Wang B.;
RT   "Cloning and analysis of adenine phosphoribosyltransferase APRT from
RT   maize.";
RL   Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY485263; AAR37033.1; -.
KW   Glycosyltransferase; Transferase.
SQ   SEQUENCE 214 AA; 22705 MW; 63BA4C4560D0B945 CRC64;

```

Alignment Scores:

Pred. No.:	5.56e-08	Length:	214
Score:	141.50	Matches:	36
Percent Similarity:	46.32%	Conservative:	8
Best Local Similarity:	37.89%	Mismatches:	49
Query Match:	24.06%	Indels:	2
DB:	2	Gaps:	1

US-09-976-054-5 (1-440) x AAR37033 (1-214)

```

QY      100 GCGATGGCGTNCGCTGATGCGCGCTTGGCGGNGATCGNCTCCTNCATCCNGGTNATNCCC 159
          ::::: ||||| ||||| ||| ||| |||
Db      34 SerLeuGlyAlaAlaAspProArgLeuGlnAlaIleSerAspAlaIleArgValValPro 53
QY      160 GACTTNCCAAAGCCAGGGATNATGTTTCAGGACATCANGANGNTGNTGTTTCGATCCCAAG 219
          ||||| ||||| ||||| |||
Db      54 HisPheProLysProGlyIleMetPheAsnAspIleThrGluLeuLeuLeuArgProGly 73

```

Qy 220 GCGNTCCGTGACAACATATACCATTTTGTCAAGCGGTACAAGGACCAAGGNATCACNTG 279
 Db 74 ValPheArgAspAlaValAspMetPheValGluArgTyrArgGlyMetGlyIleAlaAla 93
 Qy 280 GAAANTAGGAGTTAAAGCTAGAGGGNTCANTTTTCGGAACAACCTANNTCTTANAANNAATT 339
 Db 94 -AlaAlaGlyIleGluAlaArgGlyPheIlePheGlyProAlaIleAlaLeuAlaIleGl 113
 Qy 340 GGTCAAAAATNGGTGNCNATTGAGGAAGCNAATNAGNTGCCA 382
 Db 113 yAlaLys---PheIleProLeuArgLysProLysLysLeuPro 126

RESULT 13

Q7X6S6

ID Q7X6S6 PRELIMINARY; PRT; 212 AA.
 AC Q7X6S6;
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE OSJNBa0014K14.10 protein (OSJNBb0116K07.3 protein).
 GN Name=OSJNBa0014K14.10; Synonyms=OSJNBb0116K07.3;
 OS Oryza sativa (japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzeae; Oryza.
 OX NCBI_TaxID=39947;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX PubMed=12447439;
 RA Feng Q., Zhang Y., Hao P., Wang S., Fu G., Huang Y., Li Y., Zhu J.,
 RA Liu Y., Hu X., Jia P., Zhang Y., Zhao Q., Ying K., Yu S., Tang Y.,
 RA Weng Q., Zhang L., Lu Y., Mu J., Lu Y., Zhang L.S., Yu Z., Fan D.,
 RA Liu X., Lu T., Li C., Wu Y., Sun T., Lei H., Li T., Hu H., Guan J.,
 RA Wu M., Zhang R., Zhou B., Chen Z., Chen L., Jin Z., Wang R., Yin H.,
 RA Cai Z., Ren S., Lv G., Gu W., Zhu G., Tu Y., Jia J., Zhang Y.,
 RA Chen J., Kang H., Chen X., Shao C., Sun Y., Hu Q., Zhang X., Zhang W.,
 RA Wang L., Ding C., Sheng H., Gu J., Chen S., Ni L., Zhu F., Chen W.,
 RA Lan L., Lai Y., Cheng Z., Gu M., Jiang J., Li J., Hong G., Xue Y.,
 RA Han B.;
 RT "Sequence and analysis of rice chromosome 4.";
 RL Nature 420:316-320(2002).
 CC -!- SIMILARITY: Belongs to the purine/pyrimidine
 CC phosphoribosyltransferase family.
 DR EMBL; AL606604; CAE02938.2; -.
 DR EMBL; AL731638; CAE05550.1; -.
 DR Gramene; Q7X6S6; -.
 DR GO; GO:0005622; C:intracellular; IEA.
 DR GO; GO:0005478; F:intracellular transporter activity; IEA.
 DR GO; GO:0006888; P:ER to Golgi transport; IEA.
 DR InterPro; IPR005764; Ade_phospho_trans.
 DR InterPro; IPR002375; Pr/py_rp_transf.
 DR InterPro; IPR000836; PRtransferase.
 DR Pfam; PF00156; Pribosyltran; 1.
 DR TIGRFAMs; TIGR01090; apt; 1.
 DR PROSITE; PS00103; PUR_PYR_PR_TRANSFER; 1.
 KW Glycosyltransferase; Transferase.
 SQ SEQUENCE 212 AA; 22708 MW; A30E4A21A8CFB958 CRC64;

Alignment Scores:

Pred. No.:	2.92e-07	Length:	212
Score:	135.50	Matches:	36
Percent Similarity:	46.32%	Conservative:	8
Best Local Similarity:	37.89%	Mismatches:	49
Query Match:	23.04%	Indels:	2
DB:	2	Gaps:	1

US-09-976-054-5 (1-440) x Q7X6S6 (1-212)

Qy	112	GCTGATGCGCGCTTGGCGGNGATCGNCTCCTNCATCCNGGTNATNCCCGACTTNCCAAAG	171
Db	36	AlaAspProArgLeuGlnAlaIleSerAspAlaIleArgValValProHisPheProLys	55
Qy	172	CCAGGGATNATGTTTCAGGACATCANGANGNTGNTGTTTCGATCCCAAGGCGNTCCGTGAC	231
		:::	
Db	56	ProGlyIleMetPheAsnAspIleThrAlaLeuLeuLeuArgProAlaAlaPheLysAsp	75
Qy	232	AACATATACCATTTTTGTCAAGCGGTACAAGGACCAAGGNATCACCNATGGAAANTAGGAGT	291
		::: ::: ::: :::	
Db	76	AlaValAspMetPheValGluArgTyrArgGlyMetArgIleAlaAla-ValAlaGlyIl	95
Qy	292	TAAAGCTAGAGGGNTCANTTTTCGGAACAACACTANNTCTTANAANNAATTGGTCAAAAATNG	351
		::: :::	
Db	95	eGluAlaArgGlyPheIlePheGlyProAlaIleAlaLeuAlaIleGlyAlaLys---Ph	114
Qy	352	GTGNCNATTGAGGAAGCNNAATNAGNTGCCANGCNAAATGATT	394
		:::	
Db	114	eIleProLeuArgLysProLysLysLeuProGlyGluValIle	128

RESULT 14

Q84P57

ID Q84P57 PRELIMINARY; PRT; 212 AA.

AC Q84P57;

DT 01-JUN-2003 (TrEMBLrel. 24, Created)

DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Adenine phosphoribosyltransferase form 2.

OS Oryza sativa (indica cultivar-group).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

OC Ehrhartoideae; Oryzeae; Oryza.

OX NCBI_TaxID=39946;

RN [1]

RP SEQUENCE FROM N.A.

RA Li J., Weng M., Wang B.;

RL Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.

CC -!- SIMILARITY: Belongs to the purine/pyrimidine

CC phosphoribosyltransferase family.

DR EMBL; AY238894; AA085795.1; -.

DR HSSP; P49435; 1G2P.

DR Gramene; Q84P57; -.

DR GO; GO:0003999; F:adenine phosphoribosyltransferase activity; IEA.

DR GO; GO:0016757; F:transferase activity, transferring glycosyl. . .; IEA.

DR GO; GO:0006168; P:adenine salvage; IEA.

DR GO; GO:0009116; P:nucleoside metabolism; IEA.

DR InterPro; IPR005764; Ade_phospho_trans.
 DR InterPro; IPR002375; Pr/py_rp_transf.
 DR InterPro; IPR000836; PRtransferase.
 DR Pfam; PF00156; Pribosyltran; 1.
 DR TIGRFAMs; TIGR01090; apt; 1.
 DR PROSITE; PS00103; PUR_PYR_PR_TRANSFER; 1.
 KW Glycosyltransferase; Transferase.
 SQ SEQUENCE 212 AA; 22708 MW; A30E4A21A8CFB958 CRC64;

Alignment Scores:

Pred. No.:	2.92e-07	Length:	212
Score:	135.50	Matches:	36
Percent Similarity:	46.32%	Conservative:	8
Best Local Similarity:	37.89%	Mismatches:	49
Query Match:	23.04%	Indels:	2
DB:	2	Gaps:	1

US-09-976-054-5 (1-440) x Q84P57 (1-212)

Qy	112	GCTGATGCGCGCTTGGCGGNGATCGNCTCCTNCATCCNGGTNATNCCCGACTTNCCAAAG	171
Db	36	AlaAspProArgLeuGlnAlaIleSerAspAlaIleArgValValProHisPheProLys	55
Qy	172	CCAGGGATNATGTTTCAGGACATCANGANGNTGNTGTTTCGATCCCAAGGCGNTCCGTGAC	231
		:::	
Db	56	ProGlyIleMetPheAsnAspIleThrAlaLeuLeuLeuArgProAlaAlaPheLysAsp	75
Qy	232	AACATATACCATTTTGTCAAGCGGTACAAGGACCAAGGNATCACCNATGGAAANTAGGAGT	291
		::: ::: ::: :::	
Db	76	AlaValAspMetPheValGluArgTyrArgGlyMetArgIleAlaAla-ValAlaGlyIl	95
Qy	292	TAAAGCTAGAGGGNTCANTTTTCGGAACAACTANNTCTTANAANNAATTGGTCAAAAATNG	351
		::: ::	
Db	95	eGluAlaArgGlyPheIlePheGlyProAlaIleAlaLeuAlaIleGlyAlaLys---Ph	114
Qy	352	GTGNCNATTGAGGAAGCNAATNAGNTGCCANGCNAATGATT	394
		::	
Db	114	eIleProLeuArgLysProLysLysLeuProGlyGluValIle	128

RESULT 15

CAE02938

ID CAE02938 PRELIMINARY; PRT; 212 AA.
 AC CAE02938;
 DT 02-MAR-2004 (TrEMBLrel. 27, Created)
 DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
 DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
 DE OSJNBa0014K14.10 protein.
 GN OSJNBa0014K14.10.
 OS Oryza sativa (japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzeae; Oryza; Oryza sativa.
 OX NCBI_TaxID=39947;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Nipponbare;
 RX MEDLINE=22337377; PubMed=12447439;

RA Feng Q., Zhang Y., Hao P., Wang S., Fu G., Huang Y., Li Y., Zhu J.,
 RA Liu Y., Hu X., Jia P., Zhang Y., Zhao Q., Ying K., Yu S., Tang Y.,
 RA Weng Q., Zhang L., Lu Y., Mu J., Lu Y., Zhang L.S., Yu Z., Fan D.,
 RA Liu X., Lu T., Li C., Wu Y., Sun T., Lei H., Li T., Hu H., Guan J.,
 RA Wu M., Zhang R., Zhou B., Chen Z., Chen L., Jin Z., Wang R., Yin H.,
 RA Cai Z., Ren S., Lv G., Gu W., Zhu G., Tu Y., Jia J., Zhang Y.,
 RA Chen J., Kang H., Chen X., Shao C., Sun Y., Hu Q., Zhang X., Zhang W.,
 RA Wang L., Ding C., Sheng H., Gu J., Chen S., Ni L., Zhu F., Chen W.,
 RA Lan L., Lai Y., Cheng Z., Gu M., Jiang J., Li J., Hong G., Xue Y.,
 RA Han B.;
 RT "Sequence and analysis of rice chromosome 4."
 RL Nature 420:316-320(2002).
 DR EMBL; AL606604; CAE02938.2; -.
 SQ SEQUENCE 212 AA; 22708 MW; A30E4A21A8CFB958 CRC64;

Alignment Scores:

Pred. No.:	2.92e-07	Length:	212
Score:	135.50	Matches:	36
Percent Similarity:	46.32%	Conservative:	8
Best Local Similarity:	37.89%	Mismatches:	49
Query Match:	23.04%	Indels:	2
DB:	2	Gaps:	1

US-09-976-054-5 (1-440) x CAE02938 (1-212)

Qy	112	GCTGATGCGCGCTTGGCGGNGATCGNCTCCTNCATCCNGGTNATNCCCGACTTNCCAAAG	171
Db	36	AlaAspProArgLeuGlnAlaIleSerAspAlaIleArgValValProHisPheProLys	55
Qy	172	CCAGGGATNATGTTTCAGGACATCANGANGNTGNTGTTTCGATCCCAAGGCGNTCCGTGAC	231
		:::	
Db	56	ProGlyIleMetPheAsnAspIleThrAlaLeuLeuLeuArgProAlaAlaPheLysAsp	75
Qy	232	AACATATAACCATTTTGTCAAGCGGTACAAGGACCAAGGNATCACCNATGGAAANTAGGAGT	291
		::: ::: ::: :::	
Db	76	AlaValAspMetPheValGluArgTyrArgGlyMetArgIleAlaAla-ValAlaGlyIl	95
Qy	292	TAAAGCTAGAGGGNTCANTTTTCGGAACAACCTANNTCTTANAANNAATTGGTCAAAAATNG	351
		::: :::	
Db	95	eGluAlaArgGlyPheIlePheGlyProAlaIleAlaLeuAlaIleGlyAlaLys---Ph	114
Qy	352	GTGNCNATTGAGGAAGCNNAATNAGNTGCCANGCNAAATGATT	394
		:::	
Db	114	eIleProLeuArgLysProLysLysLeuProGlyGluValIle	128

Search completed: December 13, 2004, 21:24:19
 Job time : 143 secs